

WE CLAIM:

1. A method of diagnosing myocardial failure in a human comprising:

obtaining a sample of myocardial tissue from a ventricle of the heart of the human;

5 quantitating the expression of α -myosin heavy chain (α -MHC), β -myosin heavy chain (β -MHC), or both in the sample; and

determining by statistical analysis if the expression of α -MHC, β -MHC, or both in the sample is significantly different than their expression in normal human ventricular myocardial tissue.

10 2. The method of Claim 1 wherein the sample is from the left ventricle of the heart.

3. The method of Claim 1 wherein the expression of α -MHC, β -MHC, or both is quantitated by:

extracting RNA from the tissue;

preparing cDNA from the RNA;

5 amplifying the cDNA coding for α -MHC, β -MHC, or both by polymerase chain reaction (PCR) using primers that hybridize to cDNA coding for α -MHC, β -MHC, or both; and

quantitating the amplified PCR product(s).

4. The method of Claim 3 wherein the primers are labeled to allow for quantitation of the amplified PCR product(s).

5. The method of Claim 3 wherein labeled nucleotides are used during the PCR to allow for quantitation of the amplified PCR product(s).

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~~6. The method of Claim 3 wherein one or more nucleic acid molecules which hybridize to the amplified PCR product(s) is added after the PCR to allow for quantitation of the amplified PCR product(s).~~

~~7. The method of Claim 3 wherein the detection of DNA of an expected size allows for quantitation of the amplified PCR product(s).~~

~~8. The method of Claim 7 wherein the primers hybridize to both the α -MHC and β -MHC cDNAs, and the method further comprises the step of contacting the amplified PCR products with a restriction enzyme that cleaves one of the products but not the other.~~

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~~9. The method of Claim 3 further comprising:
providing an internal standard cRNA;
simultaneously preparing cDNA from the internal standard cRNA and the RNA from the sample; and
simultaneously amplifying the cDNA prepared from the internal standard cRNA and the cDNA prepared from the RNA from the sample.~~

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~~10. The method of Claim 3 wherein the expression of α -MHC and the expression of β -MHC both are determined, and the ratio of the α -MHC expression to β -MHC expression or to total α -MHC and β -MHC expression is calculated.~~

~~11. The method of Claim 10 wherein the primers hybridize to both α -MHC and β -MHC cDNAs, and the method further comprises:~~

~~5 contacting the amplified PCR products with a restriction enzyme that cleaves one of the products but not the other;~~

separating the cleaved and uncleaved PCR products by size; and
quantitating the separated PCR products.

12. A kit for diagnosing myocardial failure in a human comprising a container holding at least one nucleic acid molecule that hybridizes to DNA or RNA coding for α -MHC, β -MHC or both.

13. The kit of Claim 12 wherein the nucleic acid molecule(s) comprise(s) one or more polymerase chain reaction primers.

14. The kit of Claim 12 wherein the one or more primers hybridize to the cDNA coding for α -MHC and to the cDNA coding for β -MHC.

15. The kit of Claim 12 wherein the one or more nucleic acids are labeled.

16. The kit of Claim 13 further comprising a second container holding an internal standard cRNA.

17. A method of treating myocardial failure in a human comprising administering an effective amount of an agent that directly causes an increase in the quantity of α -myosin heavy chain (α -MHC) in the myocardial tissue of the heart

18. The method of Claim 17 wherein the agent is thyroid hormone or an analog thereof.

19. The method of Claim 17 wherein the myocardial tissue is located in a ventricle of the heart.

20. The method of Claim 19 wherein the myocardial tissue is located in the left ventricle.

21. The method of Claim 17 wherein the myocardial failure occurs in a human suffering from heart failure.

22. The method of Claim 17 wherein the myocardial failure occurs in an aging human.

Sub B² 23. The method of Claim 17 wherein the agent is a transgene coding for α -MHC.

24. A method of quantitating the expression of a first protein relative to the expression of a second protein or to the total expression of the first and second proteins comprising:

5 obtaining a sample of cells or tissue expressing the first protein and the second protein;
 extracting RNA from the cells or tissue;
 preparing cDNA from the RNA;
 amplifying the cDNA coding for the first and second
10 proteins by polymerase chain reaction (PCR) using primers that hybridize to cDNA coding for the first protein, the second protein or both; and
 quantitating the amplified PCR products.

25. The method of Claim 24 wherein one pair of primers is used, and the primers hybridize to both the cDNA coding for the first protein and the cDNA coding for the second protein.

26. The method of Claim 25 further comprising:

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contacting the amplified PCR products with a restriction enzyme that cleaves one of the products but not the other; separating the cleaved and uncleaved PCR products by size; and quantitating the separated PCR products.

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